

BLASTP 2.2.20+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: YSX8TCPP011

Database: Non-redundant SwissProt sequences
383,955 sequences; 142,559,671 total letters

Query=
Length=16

No significant similarity found. For reasons why, [click here](#).

Database: Non-redundant SwissProt sequences

Posted date: Apr 17, 2009 6:11 PM

Number of letters in database: 43,926

Number of sequences in database: 583

Lambda	K	H	
0.335	0.297	1.50	

Gapped			
Lambda	K	H	
0.294	0.110	0.610	

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Sequences: 583

Number of Hits to DB: 4781

Number of extensions: 261

Number of successful extensions: 261

Number of sequences better than 200000: 161

Number of HSP's better than 200000 without gapping: 0

Number of HSP's gapped: 228

Number of HSP's successfully gapped: 214

Length of query: 16

Length of database: 43926

Length adjustment: 6

Effective length of query: 10

Effective length of database: 40428

Effective search space: 404280

Effective search space used: 404280

T: 11

A: 40

X1: 1 (0.5 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 1 (3.6 bits)

S2: 0 (3.2 bits)